WHAT IS CLAIMED:

SUB A1

1. A method of treating a human cancer patient, comprising:

administering to the patient, one or more antisense oligomers directed to an mRNA preferentially expressed in stem cells, wherein said administering is effective to (i) increase the number of lineage committed progenitor cells and their progeny in the peripheral circulation of the subject, and/or (ii) effect a slowing or diminution of the growth of cancer cells or a solid tumor, or a reduction in the total number of cancer cells or total tumor burden in the patient.

SUB D1

2. The method of claim 1, wherein said mRNA preferentially expressed in stem cells is transcribed from a human gene selected from the group consisting of an EVI-1 zinc finger gene, a serum deprivation response (SDR) gene, a multimerin gene, a tissue transglutaminase gene, an FE65 gene, a RAB27 gene, a Jagged2 gene, a Notch1 gene, a Notch2 gene and a Notch3 gene.

3. The method of claim 1, wherein said one or more antisense oligomers has a length of about 12 to 25 bases.

SUB B

4. The method of claim 1, wherein said one or more antisense oligomers is characterized by,

(a) a backbone which is substantially uncharged;

(b) the ability to hybridize with the complementary sequence of a target RNA with high affinity at a Tm greater than 50°C;

(c) nuclease resistance; and

(d) the capability for active or facilitated transport into cells.

5. The method of claim 1, wherein said antisense oligomer backbone has a structure selected from the group consisting of the structures presented in Figures 2 A-A through 2 E-E.

6. The method according to claim 2, wherein said one or more antisense oligomers has a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:10, SEQ ID NO:11 and SEQ ID NO:12.

7. The method according to claim 6, wherein said one or more antisense oligomers has the sequence presented as SEQ ID NO:1.

SUB A2

8. The method according to any one of claims 1 to 7, wherein said one or more antisense oligomers is administered in an amount sufficient to result in a peak blood concentration of at least 200-400 nM.

9. The method according to claim 1, wherein said administering is carried out at a concentration of said one or more antisense oligomers, and for a period of time sufficient to increase the number of lineage committed progenitor cells and their progeny in the peripheral circulation of the patient at least four-fold relative to the number of lineage committed progenitor

cells and their progeny present in the peripheral blood of the patient prior to administration of said one or more antisense oligomers.

10. A method of treating a human cancer patient, comprising:

(a) obtaining a stem cell-containing cell population from a subject;

(b) treating the cell population in manner effective to enrich the cell population for stem cells; and

(c) exposing the enriched stem cell population, *ex vivo* to one or more antisense oligomers directed to an mRNA preferentially expressed in stem cells, under conditions effective to (i) to increase the population of lineage committed progenitor cells and their progeny in the peripheral circulation of the subject, and/or (ii) effect a slowing or diminution of the growth of cancer cells or a solid tumor, or a reduction in the total number of cancer cells or total tumor burden in the cell population; and

(d) infusing the antisense oligomer-treated cell population into said human cancer patient.

11. The method according to claim 10, wherein said mRNA preferentially expressed in stem cells is transcribed from a human gene selected from the group consisting of an EVI-1 zinc finger gene, a serum deprivation response (SDR) gene, a multimerin gene, a tissue transglutaminase gene, an FE65 gene, a RAB27 gene, a Jagged2 gene, a Notch1 gene, a Notch2 gene and a Notch3 gene.

12. The method according to claim 10, wherein said one or more antisense oligomers have a length of about 12 to 25 bases.

13. The method according to claim 10, wherein said one or more antisense oligomers are characterized by,

(a) a backbone which is substantially uncharged;

(b) the ability to hybridize with the complementary sequence of a target RNA with high affinity at a Tm greater than 50°C;

(c) nuclease resistance; and

(d) the capability for active or facilitated transport into cells.

14. The method according to claim 10, wherein said antisense oligomer backbone has a structure selected from the group consisting of the structures presented in Figures 2 A-A through 2 E-E.

15. The method according to claim 11, wherein said one or more antisense oligomers have a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:10, SEQ ID NO:11 and SEQ ID NO:12.

16. The method according to claim 15, wherein said antisense compound has the sequence presented as SEQ ID NO:1.

17. A composition comprising an antisense oligomer directed to a sequence spanning the mRNA translational start codon of a gene preferentially expressed in stem cells.

18. The composition according to claim 17, wherein said antisense oligomer is characterized by,

(a) a backbone which is substantially uncharged;

(b) the ability to hybridize with the complementary sequence of a target RNA with high affinity at a Tm greater than 50°C;

(c) nuclease resistance; and

(d) the capability for active or facilitated transport into cells.

19. The composition according to claim 18, wherein said antisense oligomer has the sequence presented as SEQ ID NO:1.

20. A pharmaceutical composition comprising the composition of claim 19.